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Philippines is the second world supplier of coconut by-products. The region has been threatened with devastating production constraints ranging from agro-climatic and weather calamities to widespread prevalence of disease/insect pests outbreaks, and increasing existence of non-bearing and senile palms in coconut plantations. To facilitate the development of resilient and outstanding varieties especially for added high-value traits, advancements in genomics and related technologies are harnessed towards their effective integration in a coconut breeding program. Coconut whole genome sequence reads were generated using 'Catigan Green Dwarf' (CATD) as the reference variety and combinations of advanced next generation sequencing (NGS) platforms. High quality genome assembly was generated and used to characterize adaptation and economically important genes i.e. candidate resistance genes, drought tolerance, productivity, and coconut oil related genes. Genome-wide and gene specific DNA markers are generated. A user-friendly database is being developed to house the coconut genome sequence data, gene/trait models and associated DNA markers.

Updates from the Philippines coconut genomics project will be presented. These include gene mining for host resistance against coconut scale insect (CSI) and screening for CSI least damaged coconut varieties, as well as characterization of coconut genes related to fruit flesh/endosperm mutations and coconut oil qualitative/quantitative traits. Significant result from initial molecular and biochemical studies that support nutritional and medicinal claims will also be presented. The unprecedented opportunities beyond basic science from these major S&T achievements in coconut and in integration with applicable new breeding technologies will be discussed.

W776: Palm Genetics and Genomics

Inbreeding Management and Optimization of Genetic Gain with Phenotypic and Genomic Selection in Oil Palm (*Elaeis guineensis*)

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Oil palm breeding relies on reciprocal recurrent selection between two heterotic groups complementary for bunch number and average bunch weight. Given the long generation interval and the limited selection intensity imposed by the progeny tests currently used in the program, genomic selection (GS) is a very promising solution for this species. However, GS also accelerates the annual increase in inbreeding in oil palm parental populations. This can generate inbreeding depression, which can be detrimental for seed production, and cause the loss of favourable alleles, which can reduce the long-term genetic progress. Here, we investigated the effect of three approaches of inbreeding management on parental inbreeding and genetic progress in hybrids. We simulated two widely used parental populations, La Mé and Deli, and four generations of selection. Inbreeding was measured in La Mé and genetic progress on hybrids bunch production. Inbreeding management in La Mé was made by: (i) mate selection, which uses the simulated annealing optimization algorithm, (ii) limiting deterministically the number of full-sibs selected and (iii) prohibiting selfings. The results showed that all methods slowed down the increase in parental inbreeding. Mate selection was also able to simultaneously increase the genetic progress. Stronger slowing-down in inbreeding were achieved with deterministic methods, in particular by selecting at best one individual per full-sib family and prohibiting selfings. However, this was associated with a decreased genetic progress. Finally, mate selection will allow oil palm breeders to control the rate of increase in inbreeding in the parental populations while maximizing the genetic gain.